

Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Canceled).

2. (Currently Amended) Method according to Claim 4 5 wherein the tandem mass spectrometer is a tandem in time mass spectrometer.

3. (Currently Amended) Method according to Claim 4 5 wherein the tandem mass spectrometer is a tandem in ~~time~~ space mass spectrometer.

4. (Currently Amended) Method according to Claim 3, wherein the tandem in space mass spectrometer comprises one of the group consisting of magnetic sector mass spectrometers, quadrupole filter mass spectrometers, ion trap mass spectrometers ~~or~~ and time-of-flight mass spectrometers.

5. (Currently Amended) Method for the acquisition of a mass spectrum containing information about sequences of a biopolymer, in a tandem mass spectrometer with an ion source for the ionization of the biopolymer by means of matrix-assisted laser desorption, the method comprising:

(a) preparing the biopolymer together with a matrix substance as a sample on a sample support;

(b) placing the sample support in the ion source;

(c) bombarding the sample on the sample support with light pulses from a pulsed laser with such a high energy density that it causes spontaneous fragmentations of a part of the biopolymer molecules whereby different ~~types~~ species of ISD fragment ions are formed;

12 (d) accelerating the ions and injecting them into ~~the~~ a first mass spectrometer of
13 a the tandem mass spectrometer;
14 (e) selecting one species of the ISD fragment ~~ion~~ ions in the first mass
15 spectrometer of the tandem mass spectrometer; ~~and~~
16 (f) fragmenting these the selected ISD fragment ions at least partially to
17 granddaughter ions by means of gas collisions (CID), surface collisions (SID)
18 photon collisions (PID) or metastable decay (LID); and
19 (g) measuring the granddaughter ions in the a second mass spectrometer of
20 the tandem mass spectrometer to form a granddaughter mass spectrum.

1 6. (Currently Amended) Method according to Claim 5, wherein the tandem mass
2 spectrometer comprises a quadrupole filter as the first mass spectrometer and a
3 time-of-flight mass spectrometer with orthogonal ion injection as the second
4 mass spectrometer.

1 7. (Original) Method according to Claim 5, wherein the tandem mass spectrometer
2 comprises two coaxially aligned time-of-flight mass spectrometers (TOF/TOF).

8. (Canceled).

1 9. (Currently Amended) Method according to Claim 5, wherein the ~~spectrum~~
2 ~~acquisition~~ formation of the granddaughter ions mass spectrum is preceded by a
3 ~~spectrum~~ an acquisition of ~~the~~ a mass spectrum of ISD fragment ions generated
4 in the ion source by the laser bombardment and wherein the mass spectrum of
5 the ISD fragment ions serves ~~to select~~ as a base for the selection of the one
6 species of ISD fragment ions for the ~~spectrum acquisition~~ formation of the
7 granddaughter ~~ion spectrum~~ mass spectrum.

1 10. (Currently Amended) Method according to Claim 9, wherein the biopolymers are
2 proteins and wherein ~~to assist in the selection of the ISD fragment ions, spectrum~~
3 ~~acquisitions of the ISD fragment ions with different matrix substances are~~

4 used more than one mass spectrum of the ISD fragment ions is acquired prior to
5 the formation of the granddaughter mass spectrum, and for each one of the mass
6 spectra of the ISD fragment ions, a different matrix substance is used to form ISD
7 fragment ions.

1 11. (Currently Amended) Method according to Claim 9, wherein the biopolymers are
2 proteins and prior to ~~a spectrum acquisition~~ the formation of the granddaughter
3 mass spectrum, cross links of the proteins are dissolved.

1 12. (Original) Method according to Claim 11, wherein disulfide bridges between
2 cysteines are dissolved by reduction and alkylation, or by oxidation.

1 13. (Currently Amended) Method for the determination of the terminal sequences of
2 a protein ~~wherein~~ using a tandem mass spectrometer, the method comprising:
3 (a) acquiring granddaughter ion mass spectra of different types species of
4 ISD fragment ion of the same fragmentation series are acquired, the method
5 comprising; each granddaughter mass spectrum being acquired by

6 (i) preparing the protein together with a matrix substance as a sample
7 on a sample support;

8 (ii) placing the sample support in the ion source;

9 (iii) bombarding the sample on the sample support with light pulses
10 from a pulsed laser with such a high energy density that it causes
11 spontaneous fragmentations of a part of the protein whereby
12 different species of ISD fragment ions are formed;

13 (iv) accelerating the ions and injecting them into a first mass
14 spectrometer of the tandem mass spectrometer;

15 (v) selecting one species of the ISD fragment ions in the first mass
16 spectrometer of the tandem mass spectrometer;

17 (vi) fragmenting the selected ISD fragment ions at least partially to
18 granddaughter ions by means of gas collisions (CID), surface

19 collisions (SID) photon collisions (PID) or metastable decay (LID);
20 and
21 (vii) measuring the granddaughter ions in a second mass spectrometer
22 of the tandem mass spectrometer to form a granddaughter mass
23 spectrum;
24 (b) comparing the granddaughter ion mass spectra to determine the terminal
25 ion series of the ~~ISD~~ fragment ions, ~~whereby the ion series are identified by the~~
26 ~~fact that one~~ fixed ion fragmentation series in the granddaughter ion spectra is
27 ~~fixed in the spectra while the other ion series appears to be shifted from~~
28 ~~spectrum to spectrum~~ that is not shifted on all of the granddaughter mass
29 spectra; and
30 (c) using the mass differences of the fixed ion fragmentation series to read
31 out the terminal sequence ~~pattern~~ of the protein ~~from the terminal ion series~~.

1 14. (Currently Amended) Method according to Claim 13, wherein a computer
2 program is used to identify the terminal fixed ion fragmentation series ~~from the~~
3 ~~measuring data of~~ in the granddaughter ion mass spectra.

1 15. (Currently Amended) Method according to Claim 14, wherein the determination
2 read out of the terminal sequence ~~pattern~~ is also performed by means of a
3 computer program.

1 16. (New) Method according to claim 5, wherein the tandem mass spectrometer is an
2 ion trap mass spectrometer and wherein the selection, fragmentation and
3 measuring of the granddaughter ions are carried out in the ion trap mass
4 spectrometer consecutively.